

R. Hutson

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RAW SEQUENCE LISTING
PATENT APPLICATION US/09/467,100

DATE: 04/14/2000
TIME: 06:39:35

INPUT SET: S35296.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

SEQUENCE LISTING

(1) General Information:

(i) APPLICANT: Coleman, Roger
Stuart, Susan G.

(ii) TITLE OF INVENTION: A NOVEL HUMAN JAK2 KINASE

(iii) NUMBER OF SEQUENCES: 5

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
(B) STREET: 3174 Porter Drive
(C) CITY: Palo Alto
(D) STATE: CA
(E) COUNTRY: US
(F) ZIP: 94304

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: DOS
(D) SOFTWARE: FastSEQ Version 1.5

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: 09/467,100
(B) FILING DATE:
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US/08/567,508
(B) FILING DATE: 05-DEC-1995

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Billings, Lucy J.
(B) REGISTRATION NUMBER: 36,749
(C) REFERENCE/DOCKET NUMBER: PF-0049US

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 650-855-0555
(B) TELEFAX: 650-845-4166

(2) INFORMATION FOR SEQ ID NO:1:

ENTERED

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/467,100DATE: 04/14/2000
TIME: 06:39:35

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(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4482 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:
(A) LIBRARY: Placenta
(B) CLONE: 179527

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CCACGCGTCC	GGTTGCCAAC	CCGCAGGCGA	CTGGGCGCTT	CATCCCACCC	TCACCCCTTT	60
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GGGAAGGACG	GGTCTGTTGT	ACCCGGGAGG	TGGAAGGAAA	AGCCGAAAGC	GGAGAAGTGT	240
GCGGGAGGGG	AGTCTCCGCG	CGGAGGNAGA	CCGGNCTCCT	CCAGTGCAGG	TTGTGCGCTG	300
GGGAGCCAGC	CASGGCAAAT	GTTCTGAAAA	AGACTCTGCA	TGGGAATGGC	CTGCCTTACG	360
ATGACAGAAA	TGGAGGGAAC	ATCCACCTCT	TCTATATATC	AGAATGGTGA	TATTTCTGGA	420
AATGCCAATT	CTATGAAGCA	AATAGATCCA	GTTCTTCAGG	TGTATCTTTA	CCATTCCCTT	480
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CGAATAAGGT	ACAGATTTTC	CAGATTTATT	CAGCAATTCA	GCCAATGCAA	AGCCACTGCC	1080
AGAAACTTGA	AACCTTAAGT	TCTTATAAAT	CTGGAAACTC	TGCAGTCTGC	CTTCTACACA	1140
GAGAAATTTG	AAGTAAAAGA	ACCTGGAAGT	GGTCCTTCAG	GTGAGGAGAT	TTTTGCAACC	1200
ATTATAATAA	CTGGAACCGG	TGGAATTCAG	TGGTCAAGAG	GGAAACATAA	AGAAAGTGAG	1260
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GAATATAAAC	ACTGTTTGAT	TACAAAAAAT	GAGAATGAAG	AGTACAACCT	CAGTGGGACA	1740
AAGAAGAACT	TCAGCAGTCT	TAAAGATCTT	TTGAATTGTT	ACCAGATGGA	AACTGTTTCG	1800
TCAGACAATA	TAATTTTCCA	GTTTACTAAA	TGCTGTCCCC	CAAAGCCAAA	AGATAAATCA	1860
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AATGAAAGCC	TTGGCCAAGG	CACTTTTTACA	AAGATTTTTTA	AAGGCGTACG	AAGAGAAGTA	2040
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CATTTGGTTT	TAAATTATGG	AGTATGTGTC	TGTGGAGACG	AGAATATTCT	GGTTCAGGAG	2220
TTTGTAATAA	TTGGATCACT	AGATACATAT	CTGAAAAAGA	ATAAAAATTG	TATAAATATA	2280
TTATGGAAAC	TTGAAGTTGC	TAAACAGTTG	GCATGGGCCA	TGCATTTTCT	AGAAGAAAAA	2340

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100	ACCCTTATTC	ATGGGAATGT	ATGTGCCAAA	AATATTCTGC	TTATCAGAGA	AGAAGACAGG	2400
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102	CCAAAGGACA	TTCTTCAGGA	GAGAATACCA	TGGGTACCAC	CTGAATGCAT	TGAAAATCCT	2520
103	AAAAATTTAA	ATTTGGCAAC	AGACAAATGG	AGTTTTGGTA	CCACTTTGTG	GGAAATCTGC	2580
104	AGTGGAGGAG	ATAAACCTCT	AAGTGCTCTG	GATTCTCAAA	GAAAGCTACA	ATTTTATGAA	2640
105	GATAGGCATC	AGCTTCCTGC	ACCAAAGTGG	GCAGAATTAG	CAAACCTTAT	AAATAATTGT	2700
106	ATGGATTATG	AACCAGATTT	CAGGCCTTCT	TTCAGAGCCA	TCATACGAGA	TCTTAACAGT	2760
107	TTGTTTACTC	CAGATTATGA	ACTATTAACA	GAAAATGACA	TGTTACCAAA	TATGAGGATA	2820
108	GGTGCCTTGG	GGTTTTCTGG	TGCCTTTGAA	GACCGGGATC	CTACACAGTT	TGAAGAGAGA	2880
109	CATTTGAAAT	TTCTACAGCA	ACTTGGCAAG	GGTAATTTTG	GGAGTGTGGA	GATGTGCCGG	2940
110	TATGACCCTC	TACAGGACAA	CACTGGGGAG	GTGGTCGCTG	TAAAAAAGCT	TCAGCATAGT	3000
111	ACTGAAGAGC	ACCTAAGAGA	CTTTGAAAGG	GAAATTGAAA	TCCTGAAATC	CCTACAGCAT	3060
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114	ATAGATCACA	TAAAACTTCT	GCAGTACACA	TCTCAGATAT	GCAAGGGTAT	GGAGTATCTT	3240
115	GGTACAAAAA	GGTATATCCA	CAGGGATCTG	GCAACGAGAA	ATATATTGGT	GGAGAACGAG	3300
116	AACAGAGTTA	AAATTGGRGA	TTTTGGGTTA	ACCAAAGTCT	TGCCACAAGA	CAAAGAATAC	3360
117	TATAAAGTAA	AAGAACCTGG	TGAAAGTCCC	ATATTCTGGT	ATGCTCCAGA	ATCACTGACA	3420
118	GAGAGCAAGT	TTTCTGTGGC	CTCAGATGTT	TGGAGCTTTG	GAGTGGTTCT	GTATGAACCT	3480
119	TTACATACAA	TTGAGAAGAG	TAAAAGTCCA	CCAGCGGAAT	TTATGCGTAT	GATTGGCAAT	3540
120	GACAAACAAG	GACAGATGAT	CGTGTTCAT	TTGATAGAAC	TTTTGAAGAA	TAATGGAAGA	3600
121	TTACCAAGAC	CAGATGGATG	CCCAGATGAG	ATCTATATGA	TCATGACAGA	ATGCTGGAAC	3660
122	AATAATGTAA	ATCAACGCCC	CTCCTTTAGG	GATCTAGCTC	TTGAGTGGGA	TCAAATAAGG	3720
123	GATAACATGG	CTGGATGAAA	GAAATGACCT	TCATTCTGAG	ACCAAAGTAG	ATTTACAGAA	3780
124	CAAAGTTTTA	TATTTACAT	TGCTGTGGAC	TATTATTACA	TATATCATTA	TTATATAAAT	3840
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126	TTTTTCTTCA	TGAGGCCACC	AGTAAAAGAC	ATTAATGAGA	ATTCTTTAGC	AAGGATTTTG	3960
127	TAAGAAGTTT	CTTAAACATT	GTCAGTTAAC	ATCACTCTTG	TCTGGCAAAA	GAAAAAAAAT	4020
128	AGACTTTTTT	AACTCAGCTT	TTTGAGACCT	GAAARAATTA	TTATGTAAAT	TTTGCAATGT	4080
129	TAAAGATGCA	CAGAATATGT	ATGTATAGTT	TTTACCACAG	TGGATGTATA	ATACCTTGGC	4140
130	ATCTTGTGTG	ATGTTTAAAC	CACATGAGGG	CTGGTGTTC	TTAATACTGT	TTTCTAATTT	4200
131	TTCCATGGTT	AATCTATAAT	TAATTACTTC	ACTAAACAAA	CAAATTAAGA	TGTTTCAGATA	4260
132	ATTGAATAAG	TACCTTTGTG	TCCTTGTTCA	TTTATATCGC	TGGCCAGCAT	TATAAGCAGG	4320
133	TGTATACTTT	TAGCTTGTAG	TTCCATGTAC	TGTAAATATT	TTTCACATAA	AGGGAACAAA	4380
134	TGTCTAGTTT	TATTTGTATA	GGAAATTTGC	CCTGACCCTA	AATAATACAT	TTTGAAATGA	4440
135	AACAAGCTTA	AAAAAAAAAA	AAAAAAAAAA	AAAAAAAAAA	AG		4482

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1132 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY:
- (B) CLONE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

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153
154 Met Gly Met Ala Cys Leu Thr Met Thr Glu Met Glu Gly Thr Ser Thr
155 1 5 10 15
156 Ser Ser Ile Tyr Gln Asn Gly Asp Ile Ser Gly Asn Ala Asn Ser Met
157 20 25 30
158 Lys Gln Ile Asp Pro Val Leu Gln Val Tyr Leu Tyr His Ser Leu Gly
159 35 40 45
160 Lys Ser Glu Ala Asp Tyr Leu Thr Phe Pro Ser Gly Glu Tyr Val Gly
161 50 55 60
162 Glu Glu Ile Cys Ile Ala Ala Ser Lys Ala Cys Gly Ile Thr Pro Val
163 65 70 75 80
164 Tyr His Asn Met Phe Ala Leu Met Ser Glu Thr Glu Arg Ile Trp Tyr
165 85 90 95
166 Pro Pro Asn His Val Phe His Ile Asp Glu Ser Thr Arg His Asn Val
167 100 105 110
168 Leu Tyr Arg Ile Arg Phe Tyr Phe Pro Arg Trp Tyr Cys Ser Gly Ser
169 115 120 125
170 Asn Arg Ala Tyr Arg His Gly Ile Ser Arg Gly Ala Glu Ala Pro Leu
171 130 135 140
172 Leu Asp Asp Phe Val Met Ser Tyr Leu Phe Ala Gln Trp Arg His Asp
173 145 150 155 160
174 Phe Val His Gly Trp Ile Lys Val Pro Val Thr His Glu Thr Gln Glu
175 165 170 175
176 Glu Cys Leu Gly Met Thr Val Leu Asp Met Met Arg Ile Ala Lys Glu
177 180 185 190
178 Asn Asp Gln Thr Pro Leu Ala Ile Tyr Asn Ser Ile Ser Tyr Lys Thr
179 195 200 205
180 Phe Leu Pro Gln Cys Ile Arg Ala Lys Ile Gln Asp Tyr His Ile Leu
181 210 215 220
182 Thr Arg Lys Arg Ile Arg Tyr Arg Phe Arg Arg Phe Ile Gln Gln Phe
183 225 230 235 240
184 Ser Gln Cys Lys Ala Thr Ala Arg Asn Leu Lys Leu Lys Tyr Leu Ile
185 245 250 255
186 Asn Leu Glu Thr Leu Gln Ser Ala Phe Tyr Thr Glu Lys Phe Glu Val
187 260 265 270
188 Lys Glu Pro Gly Ser Gly Pro Ser Gly Glu Glu Ile Phe Ala Thr Ile
189 275 280 285
190 Ile Ile Thr Gly Asn Gly Gly Ile Gln Trp Ser Arg Gly Lys His Lys
191 290 295 300
192 Glu Ser Glu Thr Leu Thr Glu Gln Asp Leu Gln Leu Tyr Cys Asp Phe
193 305 310 315 320
194 Pro Asn Ile Ile Asp Val Ser Ile Lys Gln Ala Asn Gln Glu Gly Ser
195 325 330 335
196 Asn Glu Ser Arg Val Val Thr Ile His Lys Gln Asp Gly Lys Asn Leu
197 340 345 350
198 Glu Ile Glu Leu Ser Ser Leu Arg Glu Ala Leu Ser Phe Val Ser Leu
199 355 360 365
200 Ile Asp Gly Tyr Tyr Arg Leu Thr Ala Asp Ala His His Tyr Leu Cys
201 370 375 380
202 Lys Glu Val Ala Pro Pro Ala Val Leu Glu Asn Ile Gln Ser Asn Cys
203 385 390 395 400
204 His Gly Pro Ile Ser Met Asp Phe Ala Ile Ser Lys Leu Lys Lys Ala
205 405 410 415

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206	Gly	Asn	Gln	Thr	Gly	Leu	Tyr	Val	Leu	Arg	Cys	Ser	Pro	Lys	Asp	Phe
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209			435					440					445			
210	Tyr	Lys	His	Cys	Leu	Ile	Thr	Lys	Asn	Glu	Asn	Glu	Glu	Tyr	Asn	Leu
211		450					455					460				
212	Ser	Gly	Thr	Lys	Lys	Asn	Phe	Ser	Ser	Leu	Lys	Asp	Leu	Leu	Asn	Cys
213	465					470					475					480
214	Tyr	Gln	Met	Glu	Thr	Val	Arg	Ser	Asp	Asn	Ile	Ile	Phe	Gln	Phe	Thr
215				485						490					495	
216	Lys	Cys	Cys	Pro	Pro	Lys	Pro	Lys	Asp	Lys	Ser	Asn	Leu	Leu	Val	Phe
217				500					505				510			
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219			515					520					525			
220	Pro	Thr	His	Met	Asn	Gln	Met	Val	Phe	His	Lys	Ile	Arg	Asn	Glu	Asp
221		530					535					540				
222	Leu	Ile	Phe	Asn	Glu	Ser	Leu	Gly	Gln	Gly	Thr	Phe	Thr	Lys	Ile	Phe
223	545					550					555					560
224	Lys	Gly	Val	Arg	Arg	Glu	Val	Gly	Asp	Tyr	Gly	Gln	Leu	His	Glu	Thr
225				565					570						575	
226	Glu	Val	Leu	Leu	Lys	Val	Leu	Asp	Lys	Ala	His	Arg	Asn	Tyr	Ser	Glu
227				580					585				590			
228	Ser	Phe	Phe	Glu	Ala	Ala	Ser	Met	Met	Ser	Lys	Leu	Ser	His	Lys	His
229			595					600					605			
230	Leu	Val	Leu	Asn	Tyr	Gly	Val	Cys	Val	Cys	Gly	Asp	Glu	Asn	Ile	Leu
231		610					615					620				
232	Val	Gln	Glu	Phe	Val	Lys	Phe	Gly	Ser	Leu	Asp	Thr	Tyr	Leu	Lys	Lys
233	625					630					635					640
234	Asn	Lys	Asn	Cys	Ile	Asn	Ile	Leu	Trp	Lys	Leu	Glu	Val	Ala	Lys	Gln
235				645						650					655	
236	Leu	Ala	Trp	Ala	Met	His	Phe	Leu	Glu	Glu	Asn	Thr	Leu	Ile	His	Gly
237				660					665				670			
238	Asn	Val	Cys	Ala	Lys	Asn	Ile	Leu	Leu	Ile	Arg	Glu	Glu	Asp	Arg	Lys
239			675					680					685			
240	Thr	Gly	Asn	Pro	Pro	Phe	Ile	Lys	Leu	Ser	Asp	Pro	Gly	Ile	Ser	Ile
241		690					695					700				
242	Thr	Val	Leu	Pro	Lys	Asp	Ile	Leu	Gln	Glu	Arg	Ile	Pro	Trp	Val	Pro
243	705					710					715					720
244	Pro	Glu	Cys	Ile	Glu	Asn	Pro	Lys	Asn	Leu	Asn	Leu	Ala	Thr	Asp	Lys
245				725					730						735	
246	Trp	Ser	Phe	Gly	Thr	Thr	Leu	Trp	Glu	Ile	Cys	Ser	Gly	Gly	Asp	Lys
247				740					745				750			
248	Pro	Leu	Ser	Ala	Leu	Asp	Ser	Gln	Arg	Lys	Leu	Gln	Phe	Tyr	Glu	Asp
249			755					760					765			
250	Arg	His	Gln	Leu	Pro	Ala	Pro	Lys	Trp	Ala	Glu	Leu	Ala	Asn	Leu	Ile
251		770					775					780				
252	Asn	Asn	Cys	Met	Asp	Tyr	Glu	Pro	Asp	Phe	Arg	Pro	Ser	Phe	Arg	Ala
253	785					790					795					800
254	Ile	Ile	Arg	Asp	Leu	Asn	Ser	Leu	Phe	Thr	Pro	Asp	Tyr	Glu	Leu	Leu
255				805						810					815	
256	Thr	Glu	Asn	Asp	Met	Leu	Pro	Asn	Met	Arg	Ile	Gly	Ala	Leu	Gly	Phe
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258	Ser	Gly	Ala	Phe	Glu	Asp	Arg	Asp	Pro	Thr	Gln	Phe	Glu	Glu	Arg	His

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Original Text